

3/8

#2



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/066,443

DATE: 03/01/2002

TIME: 10:53:13

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\03012002\J066443.raw

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3 <110> APPLICANT: Spiegelman, Bruce
4   Yoon, Cliff
6 <120> TITLE OF INVENTION: Methods and Compositions for Modulating Gluconeogenesis
7   Using PGC-1
9 <130> FILE REFERENCE: DFN-038
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/066,443
C--> 12 <141> CURRENT FILING DATE: 2002-02-05
14 <150> PRIOR APPLICATION NUMBER: 60/266,765
15 <151> PRIOR FILING DATE: 2001-02-05
17 <160> NUMBER OF SEQ ID NOS: 5
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 3066
23 <212> TYPE: DNA
24 <213> ORGANISM: Mus musculus
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28 <222> LOCATION: (92)..(2482)
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34                                     Met Ala Trp Asp Met Cys Ser
35                                     1 5
37 caa gac tct gta tgg agt gac ata gag tgt gct gct ctg gtt ggt gag 160
38 Gln Asp Ser Val Trp Ser Asp Ile Glu Cys Ala Ala Leu Val Gly Glu
39 10 15 20
41 gac cag cct ctt tgc cca gat ctt cct gaa ctt gac ctt tct gaa ctt 208
42 Asp Gln Pro Leu Cys Pro Asp Leu Pro Glu Leu Asp Leu Ser Glu Leu
43 25 30 35
45 gat gtg aat gac ttg gat aca gac agc ttt ctg ggt gga ttg aag tgg 256
46 Asp Val Asn Asp Leu Asp Thr Asp Ser Phe Leu Gly Gly Leu Lys Trp
47 40 45 50 55
49 tgt agc gac caa tcg gaa atc ata tcc aac cag tac aac aat gag cct 304
50 Cys Ser Asp Gln Ser Glu Ile Ile Ser Asn Gln Tyr Asn Asn Glu Pro
51 60 65 70
53 gcg aac ata ttt gag aag ata gat gaa gag aat gag gca aac ttg cta 352
54 Ala Asn Ile Phe Glu Lys Ile Asp Glu Glu Asn Glu Ala Asn Leu Leu
55 75 80 85
57 gcg gtc ctc aca gag aca ctg gac agt ctc ccc gtg gat gaa gac gga 400
58 Ala Val Leu Thr Glu Thr Leu Asp Ser Leu Pro Val Asp Glu Asp Gly
59 90 95 100
61 ttg ccc tca ttt gat gca ctg aca gat gga gcc gtg acc act gac aac 448
62 Leu Pro Ser Phe Asp Ala Leu Thr Asp Gly Ala Val Thr Thr Asp Asn

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63      105      110      115
65 gag gcc agt cct tcc tcc atg cct gac ggc acc cct ccc cct cag gag 496
66 Glu Ala Ser Pro Ser Ser Met Pro Asp Gly Thr Pro Pro Pro Gln Glu
67 120      125      130      135
69 gca gaa gag ccg tct cta ctt aag aag ctc tta ctg gca cca gcc aac 544
70 Ala Glu Glu Pro Ser Leu Leu Lys Lys Leu Leu Leu Ala Pro Ala Asn
71      140      145      150
73 act cag ctc agc tac aat gaa tgc agc ggt ctt agc act cag aac cat 592
74 Thr Gln Leu Ser Tyr Asn Glu Cys Ser Gly Leu Ser Thr Gln Asn His
75      155      160      165
77 gca gca aac cac acc cac agg atc aga aca aac cct gcc att gtt aag 640
78 Ala Ala Asn His Thr His Arg Ile Arg Thr Asn Pro Ala Ile Val Lys
79      170      175      180
81 acc gag aat tca tgg agc aat aaa gcg aag agc att tgt caa cag caa 688
82 Thr Glu Asn Ser Trp Ser Asn Lys Ala Lys Ser Ile Cys Gln Gln Gln
83      185      190      195
85 aag cca caa aga cgt ccc tgc tca gag ctt ctc aag tat ctg acc aca 736
86 Lys Pro Gln Arg Arg Pro Cys Ser Glu Leu Leu Lys Tyr Leu Thr Thr
87 200      205      210      215
89 aac gat gac cct cct cac acc aaa ccc aca gaa aac agg aac agc agc 784
90 Asn Asp Asp Pro Pro His Thr Lys Pro Thr Glu Asn Arg Asn Ser Ser
91      220      225      230
93 aga gac aaa tgt gct tcc aaa aag aag tcc cat aca caa ccg cag tcg 832
94 Arg Asp Lys Cys Ala Ser Lys Lys Lys Ser His Thr Gln Pro Gln Ser
95      235      240      245
97 caa cat gct caa gcc aaa cca aca act tta tct ctt cct ctg acc cca 880
98 Gln His Ala Gln Ala Lys Pro Thr Thr Leu Ser Leu Pro Leu Thr Pro
99      250      255      260
101 gag tca cca aat gac ccc aag ggt tcc cca ttt gag aac aag act att 928
102 Glu Ser Pro Asn Asp Pro Lys Gly Ser Pro Phe Glu Asn Lys Thr Ile
103      265      270      275
105 gag cga acc tta agt gtg gaa ctc tct gga act gca ggc cta act cct 976
106 Glu Arg Thr Leu Ser Val Glu Leu Ser Gly Thr Ala Gly Leu Thr Pro
107 280      285      290      295
109 ccc aca act cct cct cat aaa gcc aac caa gat aac cct ttc aag gct 1024
110 Pro Thr Thr Pro Pro His Lys Ala Asn Gln Asp Asn Pro Phe Lys Ala
111      300      305      310
113 tcg cca aag ctg aag ccc tct tgc aag acc gtg gtg cca ccg cca acc 1072
114 Ser Pro Lys Leu Lys Pro Ser Cys Lys Thr Val Val Pro Pro Pro Thr
115      315      320      325
117 aag agg gcc cgg tac agt gag tgt tct ggt acc caa ggc agc cac tcc 1120
118 Lys Arg Ala Arg Tyr Ser Glu Cys Ser Gly Thr Gln Gly Ser His Ser
119      330      335      340
121 acc aag aaa ggg ccc gag caa tct gag ttg tac gca caa ctc agc aag 1168
122 Thr Lys Lys Gly Pro Glu Gln Ser Glu Leu Tyr Ala Gln Leu Ser Lys
123      345      350      355
125 tcc tca ggg ctc agc cga gga cac gag gaa agg aag act aaa cgg ccc 1216
126 Ser Ser Gly Leu Ser Arg Gly His Glu Glu Arg Lys Thr Lys Arg Pro
127 360      365      370      375

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130 Ser Leu Arg Leu Phe Gly Asp His Asp Tyr Cys Gln Ser Leu Asn Ser
131 380 385 390
133 aaa acg gat ata ctc att aac ata tca cag gag ctc caa gac tct aga 1312
134 Lys Thr Asp Ile Leu Ile Asn Ile Ser Gln Glu Leu Gln Asp Ser Arg
135 395 400 405
137 caa cta gac ttc aaa gat gcc tcc tgt gac tgg cag ggg cac atc tgt 1360
138 Gln Leu Asp Phe Lys Asp Ala Ser Cys Asp Trp Gln Gly His Ile Cys
139 410 415 420
141 tct tcc aca gat tca ggc cag tgc tac ctg aga gag act ttg gag gcc 1408
142 Ser Ser Thr Asp Ser Gly Gln Cys Tyr Leu Arg Glu Thr Leu Glu Ala
143 425 430 435
145 agc aag cag gtc tct cct tgc agc acc aga aaa cag ctc caa gac cag 1456
146 Ser Lys Gln Val Ser Pro Cys Ser Thr Arg Lys Gln Leu Gln Asp Gln
147 440 445 450 455
149 gaa atc cga gcg gag ctg aac aag cac ttc ggt cat ccc tgt caa gct 1504
150 Glu Ile Arg Ala Glu Leu Asn Lys His Phe Gly His Pro Cys Gln Ala
151 460 465 470
153 gtg ttt gac gac aaa tca gac aag acc agt gaa cta agg gat ggc gac 1552
154 Val Phe Asp Asp Lys Ser Asp Lys Thr Ser Glu Leu Arg Asp Gly Asp
155 475 480 485
157 ttc agt aat gaa caa ttc tcc aaa cta cct gtg ttt ata aat tca gga 1600
158 Phe Ser Asn Glu Gln Phe Ser Lys Leu Pro Val Phe Ile Asn Ser Gly
159 490 495 500
161 cta gcc atg gat ggc cta ttt gat gac agt gaa gat gaa agt gat aaa 1648
162 Leu Ala Met Asp Gly Leu Phe Asp Asp Ser Glu Asp Glu Ser Asp Lys
163 505 510 515
165 ctg agc tac cct tgg gat ggc acg cag ccc tat tca ttg ttc gat gtg 1696
166 Leu Ser Tyr Pro Trp Asp Gly Thr Gln Pro Tyr Ser Leu Phe Asp Val
167 520 525 530 535
169 tcg cct tct tgc tct tcc ttt aac tct ccg tgt cga gac tca gtg tca 1744
170 Ser Pro Ser Cys Ser Ser Phe Asn Ser Pro Cys Arg Asp Ser Val Ser
171 540 545 550
173 cca ccg aaa tcc tta ttt tct caa aga ccc caa agg atg cgc tct cgt 1792
174 Pro Pro Lys Ser Leu Phe Ser Gln Arg Pro Gln Arg Met Arg Ser Arg
175 555 560 565
177 tca aga tcc ttt tct cga cac agg tcg tgt tcc cga tca cca tat tcc 1840
178 Ser Arg Ser Phe Ser Arg His Arg Ser Cys Ser Arg Ser Pro Tyr Ser
179 570 575 580
181 agg tca aga tca agg tcc cca ggc agt aga tcc tct tca aga tcc tgt 1888
182 Arg Ser Arg Ser Arg Ser Pro Gly Ser Arg Ser Ser Ser Arg Ser Cys
183 585 590 595
185 tac tac tat gaa tca agc cac tac aga cac cgc aca cac cgc aat tct 1936
186 Tyr Tyr Tyr Glu Ser Ser His Tyr Arg His Arg Thr His Arg Asn Ser
187 600 605 610 615
189 ccc ttg tat gtg aga tca cgt tca agg tca ccc tac agc cgt agg ccc 1984
190 Pro Leu Tyr Val Arg Ser Arg Ser Arg Ser Pro Tyr Ser Arg Arg Pro
191 620 625 630
193 agg tac gac agc tat gaa gcc tat gag cac gaa agg ctc aag agg gat 2032

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194 Arg Tyr Asp Ser Tyr Glu Ala Tyr Glu His Glu Arg Leu Lys Arg Asp
195          635          640          645
197 gaa tac cgc aaa gag cac gag aag cgg gag tct gaa agg gcc aaa cag 2080
198 Glu Tyr Arg Lys Glu His Glu Lys Arg Glu Ser Glu Arg Ala Lys Gln
199          650          655          660
201 aga gag agg cag aag cag aaa gca att gaa gag cgc cgt gtg att tac 2128
202 Arg Glu Arg Gln Lys Gln Lys Ala Ile Glu Glu Arg Arg Val Ile Tyr
203          665          670          675
205 gtt ggt aaa atc aga cct gac aca acg cgg aca gaa ttg aga gac cgc 2176
206 Val Gly Lys Ile Arg Pro Asp Thr Thr Arg Thr Glu Leu Arg Asp Arg
207 680          685          690          695
209 ttt gaa gtt ttt ggt gaa att gag gaa tgc acc gta aat ctg cgg gat 2224
210 Phe Glu Val Phe Gly Glu Ile Glu Glu Cys Thr Val Asn Leu Arg Asp
211          700          705          710
213 gat gga gac agc tat ggt ttc atc acc tac cgt tac acc tgt gac gct 2272
214 Asp Gly Asp Ser Tyr Gly Phe Ile Thr Tyr Arg Tyr Thr Cys Asp Ala
215          715          720          725
217 ttc gct gct ctt gag aat gga tat act tta cgc agg tcg aac gaa act 2320
218 Phe Ala Ala Leu Glu Asn Gly Tyr Thr Leu Arg Arg Ser Asn Glu Thr
219          730          735          740
221 gac ttc gag ctg tac ttt tgt gga cgg aag caa ttt ttc aag tct aac 2368
222 Asp Phe Glu Leu Tyr Phe Cys Gly Arg Lys Gln Phe Phe Lys Ser Asn
223          745          750          755
225 tat gca gac cta gat acc aac tca gac gat ttt gac cct gct tcc acc 2416
226 Tyr Ala Asp Leu Asp Thr Asn Ser Asp Asp Phe Asp Pro Ala Ser Thr
227 760          765          770          775
229 aag agc aag tat gac tct ctg gat ttt gat agt tta ctg aag gaa gct 2464
230 Lys Ser Lys Tyr Asp Ser Leu Asp Phe Asp Ser Leu Leu Lys Glu Ala
231          780          785          790
233 cag aga agc ttg cgc agg taacgtgttc ccaggctgag gaatgacaga 2512
234 Gln Arg Ser Leu Arg Arg
235          795
237 gagatgggtca atacctcatg ggacagcgtg tcctttccca agactcttgc aagtcatact 2572
239 taggaatttc tcctacttta cactctctgt acaaaaaataa aacaaaaaca aacaacaata 2632
241 acaacaacaa caacaacaat aacaacaaca accataccag aacaagaaca acggtttaca 2692
243 tgaacacagc tgctgaagag gcaagagaca gaatgataat ccagtaagca cacgtttatt 2752
245 cacgggtgtc agctttgctt tccctggagg ctcttggtga cagtgtgtgt gcgtgtgtgt 2812
247 gtgtgggtgt gcgtgtgtgt atgtgtgtgt gtgtacttgt ttggaaagta catatgtaca 2872
249 catgtgagga cttggggggc cctgaacaga acgaacaagg gcgacccctt caaatggcag 2932
251 catttccatg aagacacact taaaacctac aacttcaaaa tgttcgtatt ctatacaaaa 2992
253 ggaaaataaaa taaatataaaa aaaaaaaaaa aaaaaactcg agagatctat gaatcgtaga 3052
255 tactgaaaaa cccc 3066
258 <210> SEQ ID NO: 2
259 <211> LENGTH: 797
260 <212> TYPE: PRT
261 <213> ORGANISM: Mus musculus
263 <400> SEQUENCE: 2
264 Met Ala Trp Asp Met Cys Ser Gln Asp Ser Val Trp Ser Asp Ile Glu
265 1 5 10 15

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267 Cys Ala Ala Leu Val Gly Glu Asp Gln Pro Leu Cys Pro Asp Leu Pro
268          20          25          30
270 Glu Leu Asp Leu Ser Glu Leu Asp Val Asn Asp Leu Asp Thr Asp Ser
271          35          40          45
273 Phe Leu Gly Gly Leu Lys Trp Cys Ser Asp Gln Ser Glu Ile Ile Ser
274          50          55          60
276 Asn Gln Tyr Asn Asn Glu Pro Ala Asn Ile Phe Glu Lys Ile Asp Glu
277 65          70          75          80
279 Glu Asn Glu Ala Asn Leu Leu Ala Val Leu Thr Glu Thr Leu Asp Ser
280          85          90          95
282 Leu Pro Val Asp Glu Asp Gly Leu Pro Ser Phe Asp Ala Leu Thr Asp
283          100         105         110
285 Gly Ala Val Thr Thr Asp Asn Glu Ala Ser Pro Ser Ser Met Pro Asp
286          115         120         125
288 Gly Thr Pro Pro Pro Gln Glu Ala Glu Glu Pro Ser Leu Leu Lys Lys
289          130         135         140
291 Leu Leu Leu Ala Pro Ala Asn Thr Gln Leu Ser Tyr Asn Glu Cys Ser
292 145          150         155         160
294 Gly Leu Ser Thr Gln Asn His Ala Ala Asn His Thr His Arg Ile Arg
295          165         170         175
297 Thr Asn Pro Ala Ile Val Lys Thr Glu Asn Ser Trp Ser Asn Lys Ala
298          180         185         190
300 Lys Ser Ile Cys Gln Gln Gln Lys Pro Gln Arg Arg Pro Cys Ser Glu
301          195         200         205
303 Leu Leu Lys Tyr Leu Thr Thr Asn Asp Asp Pro Pro His Thr Lys Pro
304          210         215         220
306 Thr Glu Asn Arg Asn Ser Ser Arg Asp Lys Cys Ala Ser Lys Lys Lys
307 225          230         235         240
309 Ser His Thr Gln Pro Gln Ser Gln His Ala Gln Ala Lys Pro Thr Thr
310          245         250         255
312 Leu Ser Leu Pro Leu Thr Pro Glu Ser Pro Asn Asp Pro Lys Gly Ser
313          260         265         270
315 Pro Phe Glu Asn Lys Thr Ile Glu Arg Thr Leu Ser Val Glu Leu Ser
316          275         280         285
318 Gly Thr Ala Gly Leu Thr Pro Pro Thr Thr Pro Pro His Lys Ala Asn
319          290         295         300
321 Gln Asp Asn Pro Phe Lys Ala Ser Pro Lys Leu Lys Pro Ser Cys Lys
322 305          310         315         320
324 Thr Val Val Pro Pro Pro Thr Lys Arg Ala Arg Tyr Ser Glu Cys Ser
325          325         330         335
327 Gly Thr Gln Gly Ser His Ser Thr Lys Lys Gly Pro Glu Gln Ser Glu
328          340         345         350
330 Leu Tyr Ala Gln Leu Ser Lys Ser Ser Gly Leu Ser Arg Gly His Glu
331          355         360         365
333 Glu Arg Lys Thr Lys Arg Pro Ser Leu Arg Leu Phe Gly Asp His Asp
334          370         375         380
336 Tyr Cys Gln Ser Leu Asn Ser Lys Thr Asp Ile Leu Ile Asn Ile Ser
337 385          390         395         400
339 Gln Glu Leu Gln Asp Ser Arg Gln Leu Asp Phe Lys Asp Ala Ser Cys

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VERIFICATION SUMMARY

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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\03012002\J066443.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3